



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Tripp, Cynthia A.
Frank, Glenn R.
Grieve, Robert B.
- (ii) TITLE OF INVENTION: NOVEL PARASITIC HELMINTH
P22U PROTEINS
- (iii) NUMBER OF SEQUENCES: 17
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Sheridan Ross P.C.
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(C) CITY: Denver
(D) STATE: CO
(E) COUNTRY: U.S.A.
(F) ZIP: 80203
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/460,428
(B) FILING DATE: 02-JUN-1995
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Connell, Gary J.
(B) REGISTRATION NUMBER: 32,020
(C) REFERENCE/DOCKET NUMBER: 2618-13-3
- (ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 913 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 3..911
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GC GAG TTA AAT AGT CGA ATT TCC GGA GTA CAC CGT AAT ACT GCA GGT

Glu	Leu	Asn	Ser	Arg	Ile	Ser	Gly	Val	His	Arg	Asn	Thr	Ala	Gly		
1				5					10					15		
GCT	TTA	CAA	CGA	TTT	GCT	CTA	AAT	GGT	CAA	AAT	ACT	CTT	AAC	GAA	GGA	95
Ala	Leu	Gln	Arg	Phe	Ala	Leu	Asn	Gly	Gln	Asn	Thr	Leu	Asn	Glu	Gly	
			20					25						30		
TCA	AGT	TAT	GAG	CCA	AAC	GGA	CTA	TTT	GTA	TTT	TCA	GCA	ATA	AAC	GGT	143
Ser	Ser	Tyr	Glu	Pro	Asn	Gly	Leu	Phe	Val	Phe	Ser	Ala	Ile	Asn	Gly	
			35					40					45			
AGC	CAT	ACT	GAT	AGC	TTA	TCT	CAG	TAT	GGT	GAA	GGA	ATA	AAT	GAA	AAT	191
Ser	His	Thr	Asp	Ser	Leu	Ser	Gln	Tyr	Gly	Glu	Gly	Ile	Asn	Glu	Asn	
		50					55					60				
TAT	CAT	TCT	GGA	ACT	AAT	TAT	TAT	GAT	GAA	GTA	GAA	TTA	AGA	GAT	AAA	239
Tyr	His	Ser	Gly	Thr	Asn	Tyr	Tyr	Asp	Glu	Val	Glu	Leu	Arg	Asp	Lys	
	65					70					75					
ACA	AAT	CAG	ACA	TCG	TAC	ATT	AAT	GGA	AAT	GAT	AAT	GGA	ATC	AAT	GGA	287
Thr	Asn	Gln	Thr	Ser	Tyr	Ile	Asn	Gly	Asn	Asp	Asn	Gly	Ile	Asn	Gly	
	80					85				90					95	
AAG	GAT	GAT	GAA	GAT	CTG	GAT	GAA	TGC	TCT	GAT	CAA	GAA	TTC	CGA	TGT	335
Lys	Asp	Asp	Glu	Asp	Leu	Asp	Glu	Cys	Ser	Asp	Gln	Glu	Phe	Arg	Cys	
				100				105						110		
CCA	TAT	CTA	GCT	AAA	ACA	CTT	TGT	GTT	CAT	TAT	TTG	AAA	ATA	TGC	GAT	383
Pro	Tyr	Leu	Ala	Lys	Thr	Leu	Cys	Val	His	Tyr	Leu	Lys	Ile	Cys	Asp	
			115					120					125			
GGT	ATT	GAT	GAT	TGT	GGT	GAT	GGA	AGT	GAT	GAA	ATG	AAC	TGT	GCT	GAT	431
Gly	Ile	Asp	Asp	Cys	Gly	Asp	Gly	Ser	Asp	Glu	Met	Asn	Cys	Ala	Asp	
		130					135					140				
GAT	GAA	GTG	ATA	ACA	TCA	ATA	AAT	GGT	AAC	GAA	TCA	ATC	AAT	ATC	AGA	479
Asp	Glu	Val	Ile	Thr	Ser	Ile	Asn	Gly	Asn	Glu	Ser	Ile	Asn	Ile	Arg	
	145					150					155					
TGT	GAT	CCG	GAT	CAA	TTT	CGA	TGT	GAA	AAT	GGA	AAA	TGT	ATC	GCA	CAA	527
Cys	Asp	Pro	Asp	Gln	Phe	Arg	Cys	Glu	Asn	Gly	Lys	Cys	Ile	Ala	Gln	
	160					165				170					175	
ATT	GAT	CGA	TGT	AAT	CGA	AAA	TAT	GAT	TGT	GAT	GAT	GGT	ACA	GAT	GAA	575
Ile	Asp	Arg	Cys	Asn	Arg	Lys	Tyr	Asp	Cys	Asp	Asp	Gly	Thr	Asp	Glu	
				180					185					190		
ACA	ACT	TGT	GAA	TAT	TTC	GTG	CAA	GCT	TTG	CAA	CAA	GCG	AGA	GGT	GTA	623
Thr	Thr	Cys	Glu	Tyr	Phe	Val	Gln	Ala	Leu	Gln	Gln	Ala	Arg	Gly	Val	
			195					200					205			
ACG	GTG	CAG	GAT	AAT	GCA	ATT	CGA	GAT	GAC	GAG	ATA	CCA	AAT	TAT	ACT	671
Thr	Val	Gln	Asp	Asn	Ala	Ile	Arg	Asp	Asp	Glu	Ile	Pro	Asn	Tyr	Thr	
		210					215					220				
GTA	TCC	ATG	GAA	CAG	AAA	TAC	GAT	CAA	GTA	AAG	GAA	GAT	AAG	GAG	CGG	719
Val	Ser	Met	Glu	Gln	Lys	Tyr	Asp	Gln	Val	Lys	Glu	Asp	Lys	Glu	Arg	
	225					230					235					
CGA	ATG	CAA	GAG	GAG	GAG	GAA	CAG	GAA	AGG	CTG	AGA	GAG	TAC	GAG	GAA	767
Arg	Met	Gln	Glu	Glu	Glu	Glu	Gln	Glu	Arg	Leu	Arg	Glu	Tyr	Glu	Glu	

240	245	250	255	
CAG ATA CAG GAA AAA TTG AGG CAG GAG GAA GAA AGA GAA CGG CAA GAA				815
Gln Ile Gln Glu Lys Leu Arg Gln Glu Glu Glu Arg Glu Arg Gln Glu				
	260	265	270	
CAG GAA AGA AGA CAA AAG GAA CGA GAA AGA ATG GAA CAA GAA AGG ATA				863
Gln Glu Arg Arg Gln Lys Glu Arg Glu Arg Met Glu Gln Glu Arg Ile				
	275	280	285	
AGA CAA GAA TAT GAT GAA AAG GAA AGA CAA AGG CAA TAT GCT GAA CAG				911
Arg Gln Glu Tyr Asp Glu Lys Glu Arg Gln Arg Gln Tyr Ala Glu Gln				
	290	295	300	
GC				913

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Glu	Leu	Asn	Ser	Arg	Ile	Ser	Gly	Val	His	Arg	Asn	Thr	Ala	Gly	Ala
1				5					10					15	
Leu	Gln	Arg	Phe	Ala	Leu	Asn	Gly	Gln	Asn	Thr	Leu	Asn	Glu	Gly	Ser
			20					25					30		
Ser	Tyr	Glu	Pro	Asn	Gly	Leu	Phe	Val	Phe	Ser	Ala	Ile	Asn	Gly	Ser
		35					40					45			
His	Thr	Asp	Ser	Leu	Ser	Gln	Tyr	Gly	Glu	Gly	Ile	Asn	Glu	Asn	Tyr
	50					55					60				
His	Ser	Gly	Thr	Asn	Tyr	Tyr	Asp	Glu	Val	Glu	Leu	Arg	Asp	Lys	Thr
65					70				75						80
Asn	Gln	Thr	Ser	Tyr	Ile	Asn	Gly	Asn	Asp	Asn	Gly	Ile	Asn	Gly	Lys
				85				90						95	
Asp	Asp	Glu	Asp	Leu	Asp	Glu	Cys	Ser	Asp	Gln	Glu	Phe	Arg	Cys	Pro
			100					105					110		
Tyr	Leu	Ala	Lys	Thr	Leu	Cys	Val	His	Tyr	Leu	Lys	Ile	Cys	Asp	Gly
		115					120					125			
Ile	Asp	Asp	Cys	Gly	Asp	Gly	Ser	Asp	Glu	Met	Asn	Cys	Ala	Asp	Asp
	130					135					140				
Glu	Val	Ile	Thr	Ser	Ile	Asn	Gly	Asn	Glu	Ser	Ile	Asn	Ile	Arg	Cys
145					150					155					160
Asp	Pro	Asp	Gln	Phe	Arg	Cys	Glu	Asn	Gly	Lys	Cys	Ile	Ala	Gln	Ile
				165					170					175	

Asp Arg Cys Asn Arg Lys Tyr Asp Cys Asp Asp Gly Thr Asp Glu Thr
 180 185 190
 Thr Cys Glu Tyr Phe Val Gln Ala Leu Gln Gln Ala Arg Gly Val Thr
 195 200 205
 Val Gln Asp Asn Ala Ile Arg Asp Asp Glu Ile Pro Asn Tyr Thr Val
 210 215 220
 Ser Met Glu Gln Lys Tyr Asp Gln Val Lys Glu Asp Lys Glu Arg Arg
 225 230 235 240
 Met Gln Glu Glu Glu Glu Gln Glu Arg Leu Arg Glu Tyr Glu Glu Gln
 245 250 255
 Ile Gln Glu Lys Leu Arg Gln Glu Glu Glu Arg Glu Arg Gln Glu Gln
 260 265 270
 Glu Arg Arg Gln Lys Glu Arg Glu Arg Met Glu Gln Glu Arg Ile Arg
 275 280 285
 Gln Glu Tyr Asp Glu Lys Glu Arg Gln Arg Gln Tyr Ala Glu Gln
 290 295 300

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1016 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
- (A) NAME/KEY: CDS
 - (B) LOCATION: 3..626

- (ix) FEATURE:
- (A) NAME/KEY: 3'UTR
 - (B) LOCATION: 627..1016

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GT TTT GTT GTA CTA CTC GTT GTT GCA ATA TGG ATT GAA ATG AGC CAA	47
Phe Val Val Leu Leu Val Val Ala Ile Trp Ile Glu Met Ser Gln	
1 5 10 15	
GGC CAA CAA ATG ATC AAA CAA TGT AAA TGT TCT GAT ATT GCA CCA TGT	95
Gly Gln Gln Met Ile Lys Gln Cys Lys Cys Ser Asp Ile Ala Pro Cys	
20 25 30	
CAA TTA ACT GCC GTT CAA TCA GTT TTA CCA TGT GCT GAT CAA TGC CAG	143
Gln Leu Thr Ala Val Gln Ser Val Leu Pro Cys Ala Asp Gln Cys Gln	
35 40 45	
AAA TAT ATT ACT TCA ATT GGT GGT AAT TAT GAT CAA ATT AGT AAC TGT	191
Lys Tyr Ile Thr Ser Ile Gly Gly Asn Tyr Asp Gln Ile Ser Asn Cys	
50 55 60	

TTT AAA CAG AAA CAA TCA ATT ATA AAT GAT GCT ATG AAA TGT GCT CAA Phe Lys Gln Lys Gln Ser Ile Ile Asn Asp Ala Met Lys Cys Ala Gln 65 70 75	239
GAT GCT TTC CCA AAT GCA TGC GCA CAA GGT GAA CCA AAA ATG GTA CCA Asp Ala Phe Pro Asn Ala Cys Ala Gln Gly Glu Pro Lys Met Val Pro 80 85 90 95	287
AAA CGA TTC GGA AAA GGT CTT CAA TTA GCT GTA ATG ACT GAT ATC AAC Lys Arg Phe Gly Lys Gly Leu Gln Leu Ala Val Met Thr Asp Ile Asn 100 105 110	335
AAA GAA TTA CAA CGA ATG GGA ATA GCA AAT CAA GTT ACT CAA CTA ATC Lys Glu Leu Gln Arg Met Gly Ile Ala Asn Gln Val Thr Gln Leu Ile 115 120 125	383
TCC CAA GGT CGA CGA TTC TTT AAA TGC TTC CAA TCG TGT ATG ATG AAA Ser Gln Gly Arg Arg Phe Phe Lys Cys Phe Gln Ser Cys Met Met Lys 130 135 140	431
AAA TTG GGC TCA TGT TCT CCA GAT TGT GGT CTT GAT TTA CCA TCT GAT Lys Leu Gly Ser Cys Ser Pro Asp Cys Gly Leu Asp Leu Pro Ser Asp 145 150 155	479
AAT GTT ATG GTT CAA ACA GTT AAA AAT TGC GCT CAA AAA AGT GGT ATT Asn Val Met Val Gln Thr Val Lys Asn Cys Ala Gln Lys Ser Gly Ile 160 165 170 175	527
CAA ACT GCA TCG GTG CAA GAT CTT TGC TTT TGC GTC GAA CAA GCT GGT Gln Thr Ala Ser Val Gln Asp Leu Cys Phe Cys Val Glu Gln Ala Gly 180 185 190	575
ATT CGG CAA CTT TCT GAT GTA TGT CCT CGT ATA CAA ATT TTC AAA ACG Ile Arg Gln Leu Ser Asp Val Cys Pro Arg Ile Gln Ile Phe Lys Thr 195 200 205	623
AAA TGAGTATTGA GAATATTGCA CTAGCAGCAA TCATTATTTT TCTCGAGAAT Lys	676
TTTCGCTATC AATAAGTTGG AATATGATTA CAATAATATA TATATTAACT GCAAAAAATCT	736
TTCTTCTTCA AAATTATTTT TCATTTTCGCT CTCATAATTG CATGATAATA GTCATAATGA	796
AAAACAGGTT TTCTTTTTTT AAAATGATAA CTTCAAACAA ATAGGTATTT CTTGATATAT	856
ATATGTATGT ATGTATGTGT GTGTGTGTGT GTGTGTGTAT GTGTGTGTTT GTGTATGTGT	916
ATATGTATGT ATGTATGTAT GTATGTATGT ATGTGTAGGA GAAAAGCAAA CTAAACAGTA	976
AATGAAAGAA AAAAATAAGT CAAATAAAAG TTTGATAATT	1016

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
Phe Val Val Leu Leu Val Val Ala Ile Trp Ile Glu Met Ser Gln Gly
 1           5           10           15
Gln Gln Met Ile Lys Gln Cys Lys Cys Ser Asp Ile Ala Pro Cys Gln
          20           25           30
Leu Thr Ala Val Gln Ser Val Leu Pro Cys Ala Asp Gln Cys Gln Lys
          35           40           45
Tyr Ile Thr Ser Ile Gly Gly Asn Tyr Asp Gln Ile Ser Asn Cys Phe
          50           55           60
Lys Gln Lys Gln Ser Ile Ile Asn Asp Ala Met Lys Cys Ala Gln Asp
          65           70           75           80
Ala Phe Pro Asn Ala Cys Ala Gln Gly Glu Pro Lys Met Val Pro Lys
          85           90           95
Arg Phe Gly Lys Gly Leu Gln Leu Ala Val Met Thr Asp Ile Asn Lys
          100          105          110
Glu Leu Gln Arg Met Gly Ile Ala Asn Gln Val Thr Gln Leu Ile Ser
          115          120          125
Gln Gly Arg Arg Phe Phe Lys Cys Phe Gln Ser Cys Met Met Lys Lys
          130          135          140
Leu Gly Ser Cys Ser Pro Asp Cys Gly Leu Asp Leu Pro Ser Asp Asn
          145          150          155          160
Val Met Val Gln Thr Val Lys Asn Cys Ala Gln Lys Ser Gly Ile Gln
          165          170          175
Thr Ala Ser Val Gln Asp Leu Cys Phe Cys Val Glu Gln Ala Gly Ile
          180          185          190
Arg Gln Leu Ser Asp Val Cys Pro Arg Ile Gln Ile Phe Lys Thr Lys
          195          200          205
```

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
Asp Asp Cys Gly Asp Gly Ser Asp Glu
 1           5
```

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Ala	Gln	Asp	Ala	Phe	Pro	Asn	Ala	Cys	Ala	Gln	Gly	Glu	Pro	Lys
1				5				10						15	

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ala	Ile	Ala	Pro	Cys	Gln	Leu	Thr	Ala	Val	Gln	Ser	Val	Leu	Pro	Cys
1				5				10						15	

Ala	Asp	Gln	Cys	Gln	Lys
			20		

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Leu	Gly	Ser	Cys	Ser	Pro	Asp	Cys	Gly	Leu	Asp	Leu	Pro	Ser	Asp	Asn
1				5				10						15	

Val	Met	Val	Gln	Asp	Val
			20		

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION: 1..23

(D) OTHER INFORMATION: /label= PRIMER

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CGGGATCCCG AGTTAAATAG TCG

23

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION: 1..17

(D) OTHER INFORMATION: /label= PRIMER

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TGCAGGATCC TGCACCG

17

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION: 1..50

(D) OTHER INFORMATION: /label= PRIMER

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GAGAGAGAGA GAGAGAGAGA ACTAGTCTCG AGTTTTTTTTT TTTTTTTTTT

50

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..17
 - (D) OTHER INFORMATION: /label= PRIMER

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TGYTCNCCNG AYTGYGG

17

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..17
 - (D) OTHER INFORMATION: /label= PRIMER

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TGYAGTCCNG AYTGYGG

17

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..17
 - (D) OTHER INFORMATION: /label= PROBE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TGNACCATNA CRTTRTC

17

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..27
 - (D) OTHER INFORMATION: /label= PROBE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CTGTTTGAAC CATAACATTA CAGATGG

27

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..25
 - (D) OTHER INFORMATION: /label= PRIMER

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GTTGCAATAT GGGATCCAAT GAGCC

25

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..25
 - (D) OTHER INFORMATION: /label= PRIMER

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CGCTAGTGCA GGATCCTCAA TACTC

25